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T H N E F T I T H V I V P -- K Q S A G P D Y C D M E N V E K L F N V Q D Q H D -- L L T L G W I E T P Q T A F L S
T H N E F T I T H V I V P -- K Q S A G P D Y C D M E N E K L F N V Q D Q H D -- L L T L G W I E T P Q T A F L S
M E N E F T I T H V L I P -- K Q S A G S D Y C N T E N E E K L F L I Q D Q G S -- L L T L G W I E T P Q T A F L S
T R V I D V F A M P Q S -- G T G V S E A V D P V F Q A K M L D M K Q T G R F E M V G W Y E S P G I G C N L S
T M I I M D S F A L P V E G T E T R V N A Q A A A Y E Y A A Y I E N A K Q V G R L E N A I G W Y E S P G Y G C N L S

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[illegible]

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TKEPRLFSICKHV--LVKDIKI-----IVLDLR-----
TKEPRLFSIQNVLGIIISGTA-----EMEPLKIGYGPNGFPLLGISRSSSPSEQ
SKDPLFLCSCSHVT--VVDRAV-----TITDLR-----
LNKPSIQALINGLNRRHYSITINYRKNELEQKMLLNTHKRSMEGLTIDQYSECHKNES
TIPLNKIEDFGVHCKQYYALEVSYFKSSLDKILLELWNKYVWNTLSSSSLLTNADYTTG

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L-----

VVKEMLELAKNYNKA VEKEDKMTPEQLAIRNVGRQDPKRHLETHVDVMTSNIVQCLAM
QVFDLSEKLEQSEAQLGRGSFMIG--LETHDRKSEDLAKATRDSCKTTIEAHHGLMSQV

LDTVVFK-----
IKDKLENDINIS

FIGURE 1

[illegible]

COP9_su5_Hs	VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm	VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_su5_At	AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVIDPTRTVSAGKVEIG
COP9_su5_Ce	EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
AF2198_Arcfu	LPIGMKVFGTVHSHPSPCRPSEEDLSLFTFRFGKYHIIVCY--PYDENSWKCYNRKGEEV
PH0451_Pyrho	MPHDESIKGTFSHSPSPFPYPSEGLMFFSKFGGIHI IAAF--PYDEDSVKAFDSEGREV
TVN1035_Thevo	KPIDFSLVGSVHSHPSGITKPSDEDLRMFSLTGKIHIIVGY--PYNLKDYSAYDRSGNKV
MTH971_Metth	LPPFTGAVGSVHSHPGPVNLPSAADLHFFSKNGLFHLI IAH--PYTMETVAAYTRNGDPV
aq_1691_Aquae	ISKGMEIVGVYHSHPDHPDRPSQFDLQRAFPDLSYII FSVQ--KGKVASYRSWELKGDKF
RV1334_Myctu	EDADEVPVVIYHSHTATEAYPSRTDVKLATEPDAHVVLVSTRDPHRHELRSYRIVDGAVT
RadC_Ecoli	IKINASALILAHNHPSGCAEPSKADKLITERIIKSCQFMDL--RVLDHIVIGRGEYVSFA
.....HSHP.....S ''D

FIGURE 3

COP9_bu5_Hs	VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm	VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_su5_At	AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQHQEPFLA--VVIDPTRTVSAGKVEIG
COP9_su5_Ce	EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
Pad1_Dm	TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Pad1_Hs	TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Skel_Dd	TGRDEIVIGWYHSHPGFGCWLSVDVNTQQSFEQLQSRAVA--VVVDPLQSVRG-KVVID
Pad1_Sc	TGRDQMVVGWYHSHPGFGCWLSVDVNTQKSFEQLNSRAVA--VVVDPIQSVKG-KVVID
.....	HSHP''''''S 'D

FIGURE 4